



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

THE APPLICATION OF:  
STEPHEN M. ALLEN

APPLICATION NO.: 09/740,288

CASE NO.: BB1429 US NA

FILED: CONCURRENTLY HEREWITH

GROUP ART UNIT: UNKNOWN

FOR: **PLANT BIOTIN SYNTHASE**

EXAMINER: UNKNOWN

Assistant Commissioner for Patents  
Washington, DC 20231

Sir:

**DECLARATION IN ACCORDANCE WITH 37 CFR 1.821**

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively are the same.

Respectfully submitted,



KENING LI  
ATTORNEY FOR APPLICANTS  
REGISTRATION NO. 44,872  
TELEPHONE: 302-992-3749  
FACSIMILE: 302-892-1026

Dated: 04/10/2001

DOCKET NO: 882014/60



#5

## SEQUENCE LISTING

<110> Allen, Stephen  
Kinney, Anthony  
Miao, Guo-Hua  
Orozco, Emil

<120> PLANT BIOTIN SYNTHASE

<130> BB1429 US NA

<140> US 09/740288  
<141> 2000-12-19

<150> US 60/172929  
<151> 1999-12-21

<160> 36

<170> Microsoft Office 97

<210> 1  
<211> 512  
<212> DNA  
<213> Hordeum vulgare

<220>  
<221> Unsure  
<222> (94)..(94)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (460)..(460)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (462)..(462)  
<223> n = A, C, G, or T

<400> 1  
caactccctc ggcagtatcg cctagtgcag cagcggtctcc gttccggccaa gctttgtctcg 60  
ccgagccggc catgtatcgct ctgcgtcgcc gcancttcgc tcccgctgc ggtccccctt 120  
cgccctccggcc gttacgcggcc cgcccttcgtc atcggatcg gggccgggg cggaggccgga 180  
cgggccgtgc gggacggggcc caggaacgac tggacccggcc cccagatccaa ggccatctac 240  
gactcccccg tcctcgaccc tctcttcacca ggggtcaag tccataggaa tgcctataaaa 300  
tttagagaaatg tgcaacaatcg cacaatcttca tcaataaaaga ctgggtgggtg cagcgaat 360  
tgttcataact gcccacatgc tcaatcgatc agtaccggat tgaaggctga aaaatataatg 420  
aagaatggatc cggctctaga agcagctaa aaggccaaagn angctggggag caccggattt 480  
tgattggagc gatggagaga gacaattggc ag 512

<210> 2  
<211> 137  
<212> PRT  
<213> Hordeum vulgare

<220>  
<221> UNSURE  
<222> (131)..(131)  
<223> Xaa = any amino acid

<400> 2  
Met Met Leu Leu Leu Ala Arg Ser Leu Arg Ser Arg Val Arg Ser Pro  
1 5 10 15  
Phe Ala Ser Ala Val Ser Ala Ala Pro Phe Ser Ser Val Ser Ala Ala  
20 25 30  
Ala Ala Glu Ala Glu Arg Ala Val Arg Asp Gly Pro Arg Asn Asp Trp  
35 40 45  
Thr Arg Pro Glu Ile Gln Ala Ile Tyr Asp Ser Pro Leu Leu Asp Leu  
50 55 60  
Leu Phe His Gly Ala Gln Val His Arg Asn Val His Lys Phe Arg Glu  
65 70 75 80  
Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu  
85 90 95  
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Leu Lys  
100 105 110  
Ala Glu Lys Leu Met Lys Lys Asp Ala Val Leu Glu Ala Ala Lys Lys  
115 120 125  
Ala Lys Xaa Ala Gly Ser Thr Arg Phe  
130 135

<210> 3  
<211> 496  
<212> DNA  
<213> Zea mays

<220>  
<221> Unsure  
<222> (33)..(33)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (318)..(318)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (321)..(321)  
<223> n = A, C, G, or T

<220>  
 <221> Unsure  
 <222> (365)..(365)  
 <223> n = A, C, G, or T

<220>  
 <221> Unsure  
 <222> (446)..(446)  
 <223> n = A, C, G, or T

<400> 3  
 tccaaatcggttgggcagttttaaggaaac cangaccgc aagcaagcaa gccgccccag 60  
 ccgacgaggc gaggagcgtt caattccgtt gctgcaacga actccctcgca ccgtatcgcc 120  
 cgtgtctctt ctatccctt cctgtctgtt ctatcaccc aagctatcac tatcatggcc 180  
 ttgatgtctgtc tagcgcgcaaa cctgcgcctt cgcctccgc caccgctcgc cgccgcgcg 240  
 gggttctctgtc cgccgcgcgc ggaggcggag agggcgatac gggacgggccc gcggaacgc 300  
 tggagccgcgc cccagatnca ngccgtctatc gactcacccgc tcctcgaccc ccttttcac 360  
 ggggnntcaagt catcaagata caacactggtt ttgaaggccc aaaaattgtat gaacaaatat 420  
 gctgtcttgg gaggcagcaaa aaaggnaaaa gagtctggga agcaaccgtt tttgcatggg 480  
 aactgcattt gagaaa 496

<210> 4  
 <211> 102  
 <212> PRT  
 <213> Zea mays

<220>  
 <221> UNSURE  
 <222> (48)..(49)  
 <223> Xaa = any amino acid

<220>  
 <221> UNSURE  
 <222> (64)..(64)  
 <223> Xaa = any amino acid

<220>  
 <221> UNSURE  
 <222> (91)..(91)  
 <223> Xaa = any amino acid

<400> 4  
 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro  
 1 5 10 15  
 Pro Leu Ala Ala Ala Ala Gly Phe Ser Ser Ala Ala Ala Glu Ala Glu  
 20 25 30  
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa  
 35 40 45  
 Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa  
 50 55 60

Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Met Asn  
 65 70 75 80  
 Lys Tyr Ala Val Leu Gly Ala Ala Lys Lys Xaa Lys Glu Ser Gly Lys  
 85 90 95  
 Gln Pro Phe Leu His Gly  
 100

<210> 5  
 <211> 497  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> Unsure  
 <222> (192)..(192)  
 <223> n = A, C, G, or T

<220>  
 <221> Unsure  
 <222> (460)..(460)  
 <223> n = A, C, G, or T

<220>  
 <221> Unsure  
 <222> (463)..(463)  
 <223> n = A, C, G, or T

<220>  
 <221> Unsure  
 <222> (469)..(469)  
 <223> n = A, C, G, or T

<220>  
 <221> Unsure  
 <222> (490)..(490)  
 <223> n = A, C, G, or T

<400> 5  
 agccgacgag gcgaggagcg tgcaattccg tagctgcAAC tgcaacgAAC tccctccctc  
 60  
 cctcgaccgt atgcggccgt gctcctctat ccctttctcg ctgtgcatac taccttaa  
 120  
 tatcatggcc ttgatgtcgc tagcgccaa cctgcgttcc cgctctccggc caccgcgtcg  
 180  
 cgccgcgcgc gngttctgt cgccgcgcgc ggaggcgag agggcgatac gggacggcc  
 240  
 gccgaacgac tggagccgc ccgagattca agccgttccat gactcacccg tcctcgacct  
 300  
 cctctttcac ggggctcaag tccacagaaa tgtccataaa ttcaagaaaa gtgcagcaat  
 360  
 gcacacttctt ttcataatcaag actgggtggaa tgcaatgtaaat ttgttcttca  
 420  
 gtcatcaaaat aataacaacac tgggattgaa gggcccaaaan aanttgatna aaaaaagatg  
 480  
 ctgtcttggn aacaaca  
 497

<210> 6

<211> 98  
<212> PRT  
<213> Zea mays

<220>  
<221> UNSURE  
<222> (23)..(23)  
<223> Xaa = any amino acid

<220>  
<221> UNSURE  
<222> (72)..(72)  
<223> Xaa = any amino acid

<220>  
<221> UNSURE  
<222> (89)..(89)  
<223> Xaa = any amino acid

<400> 6  
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro  
1 5 10 15  
Pro Leu Ala Ala Ala Ala Xaa Phe Ser Ser Ala Ala Ala Glu Ala Glu  
20 25 30  
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile  
35 40 45  
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala  
50 55 60  
Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr  
65 70 75 80  
Leu Leu Ser Ile Lys Thr Gly Gly Xaa Ser Glu Asp Cys Ser Tyr Cys  
85 90 95  
Pro Gln

<210> 7  
<211> 1152  
<212> DNA  
<213> Zea mays

<400> 7  
gcagccgacg aggccgaggag cgtcaattc cgtagctgca acgaaactccc tcgaccgtat 60  
cgcccgctgc tcctctatcc ctttctgtt gctgtctacta cttttaagctta tcactatcat 120  
ggcccttgatg ctgtctagcgc gcaacctggcg ctcccgccctc cgccccacccgc tcggccggcg 180  
cgccggcttc tctggccggc cggccggagc ggagaggggcg atacgggacg ggccggccgaa 240  
cgactggagc cggcccgaga tccaggccgt ctacgactca ccgtctctcg acctctctct 300  
tcaacggggat cagggtccaca gaaatgtccca taaaattcaga gaatgtcaga aatgcacact 360  
tctttcaatc aagactgggt gatgcagtga agatgtttt tactgtctc agtcatcaag 420  
ataacaacatc ggatgttggaaatc gatgttgcataa tatgtcttctt tggaaagcagc 480  
aaaaaaaggca aaagactgtc ggagaccccg tttttgcatc ggagctgcat ggagagaaac 540  
cattggcagg aaatcaaact tcaaccagat tcttgcataat gtcagaaggaa taaggggat 600  
ggggatggag gtctgttgc aactaggat gatagagaaaa caacaactgt aagaactcaa 660

gaaggctgga	cttacacgat	ataatcataa	cctagataca	tcaagagagt	attatccaa	720
cattatttac	acaaagatcat	atgatgatag	atgcgcact	cttgcgcatg	tccgtgaagc	780
tggaaatacg	atctgcctcg	gttgaatcat	tgttcttgg	gaagcagagg	aggacgggt	840
agggttgtg	cataccctag	ctaccctggc	tacacaccca	gagagcgttc	ctattaatgc	900
atgggttgc	gtaaaaggca	caccttta	ggaccagaag	cctgttagaga	tctggaaat	960
gatccgcat	atgcgcact	ctcgatcac	gatgcggaaag	gcaatggta	ggcttcagc	1020
aggccgat	cggttctcg	tgccagaaca	agcgcgtgc	ttccctcgctg	gggcacactc	1080
catccttgc	ggcgagaaac	ttctcacaac	cgccaaacaa	gactttatgc	cggaccaagc	1140
gatgttcaag	at					1152

<210> 8  
<211> 344  
<212> PRT  
<213> Zea mays

<400> 8						
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg	Leu Arg Pro					
1	5	10	15			
Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala	Glu Ala Glu					
20	25	30				
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg	Pro Glu Ile					
35	40	45				
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe	His Gly Ala					
50	55	60				
Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln	Gln Cys Thr					
65	70	75	80			
Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys	Ser Tyr Cys					
85	90	95				
Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln	Lys Leu Met					
100	105	110				
Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys	Glu Ser Gly					
115	120	125				
Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr	Ile Gly Arg					
130	135	140				
Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu	Ile Arg Gly					
145	150	155	160			
Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu	Lys Gln Gln					
165	170	175				
Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn	His Asn Leu					
180	185	190				
Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr	Arg Ser Tyr					
195	200	205				
Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala	Gly Ile Ser					
210	215	220				
Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu	Glu Asp Arg					
225	230	235	240			
Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His	Pro Glu Ser					
245	250	255				
Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro	Leu Glu Asp					
260	265	270				
Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile	Ala Thr Ala					
275	280	285				
Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala	Gly Arg Val					
290	295	300				
Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala	Gly Ala Asn					

305	310	315	320
Ser Ile Leu Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe			
	325	330	335
Asp Ala Asp Gln Ala Met Phe Lys			
	340		

```
<210> 9
<211> 562
<212> DNA
<213> Argemone mexicana
```

<220>  
<221> Unsure  
<222> (553)..(553)  
<223>  $n = A, C, G, \text{ or } T$

```

<400> 9
cattcgagaa ataaaagact gtaaaattt tagggtttt ctgcataact ctacactcga 60
atggctcatc ataaaaatat cataaacaga agaattcaa atgcttaaaat tcaatcttt 120
gagagetcgt cttcgacctt tgatttcat ttctacattt tttttctctt catcatcttc 180
ttcttcataa gctgtgtgtc ttacagcaga aagaacgatt aagaacggtc caagaaacga 240
ttggcagaca gatggaaat aatcgggtt tgatgttcca gtttcgttcc ttcttccttca 300
tgcagctcaa gtccatagac atgtccacaa cttcggggaa gtgcggcaat gtaactttctt 360
ctctttttaa acagggtgggt gcagtgaaaga ttgttcatat ttccacaaat ttcccgatgt 420
tgacacttgg a gtaaaaggccc aaaaagctgtat gaaacaaggga cggcgttctgtc caaggaagca 480
agaaaaaggca aaggggggccgg tggtatcac gtttcgcaat tggtggctgc aatggggaga 540
ttaataatggg aaaaadaaacaa aa 562

```

<210> 10  
<211> 119  
<212> PRT  
<213> *Argemone mexicana*

```

<400> 10
Met Leu Lys Val Glu Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe
      5          10          15
Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ala Ala
      20          25          30
Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
      35          40          45
Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
      50          55          60
Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
      65          70          75          80
Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
      85          90          95
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
      100         105         110
Ala Gln Lys Leu Met Asn Lys
      115

```

<210> 11

```

<210> 12
<211> 374
<212> PRT
<213> Glycine max

<400> 12
Met Phe Leu Ala Arg Pro Ile Phe Arg Ala Pro Ser Leu Trp Ala Leu
          5          10          15
His Ser Ser Tyr Ala Tyr Ser Ser Ala Ser Ala Ala Ala Ile Gln Ala
          20          25          30
Glu Arg Ala Ile Lys Glu Gly Pro Arg Asn Asp Trp Ser Arg Asp Gln
          35          40          45
Val Lys Ser Ile Tyr Asp Ser Pro Ile Leu Asp Leu Leu Phe His Gly
          50          55          60
Ala Gln Val His Arg His Ala His Asn Phe Arg Glu Val Gln Gln Cys
          65          70          75          80
Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr
          85          90          95
Cys Pro Gln Ser Ser Lys Tyr Asp Thr Gly Val Lys Arg Pro Ser Leu
          100         105         110
Met Asn Lys Glu Ala Val Leu Gln Ala Ala Lys Lys Ala Lys Glu Ala
          115         120         125
Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Thr Leu Gly
          130         135         140
Arg Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg
          145         150         155         160

```

Asp Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln  
 165 170 175  
 Gln Ala Val Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn  
 180 185 190  
 Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Thr  
 195 200 205  
 Tyr Asp Glu Arg Leu Gln Thr Leu Glu Phe Val Arg Asp Ala Gly Ile  
 210 215 220  
 Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp  
 225 230 235 240  
 Arg Val Gly Leu Leu His Thr Leu Ser Thr Leu Pro Thr His Pro Glu  
 245 250 255  
 Ser Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu  
 260 265 270  
 Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr  
 275 280 285  
 Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg  
 290 295 300  
 Val Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala  
 305 310 315 320  
 Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr Pro Asn Asn Asp  
 325 330 335  
 Phe Asp Ala Asp Gln Leu Met Phe Lys Val Leu Gly Leu Leu Pro Lys  
 340 345 350  
 Ala Pro Ser Leu His Glu Gly Glu Thr Ser Val Thr Glu Asp Tyr Lys  
 355 360 365  
 Glu Ala Ala Ser Ser Ser  
 370

<210> 13  
 <211> 479  
 <212> DNA  
 <213> Glycine max

<400> 13  
 ggcaacttc agaacttccc tatcacgata cctcatcctc cttcgctcca atacccttaa 60  
 atcgcacccat atcttttctt ctgttcgtct tcaagtccaa aagtgcagaa actatggtaa 120  
 cgtatcatct gttcttcctc aagctacaga aacatcaagc acatcaccta gtaaggatct 180  
 ctacaagaa gcaactcaacg caactgaacc cccgagcaat tggacaagag aagaaatcaa 240  
 ggcgatctt gataggccat tggatgggtt atgttgggggt gctggtagtt tgacaggaa 300  
 attccatata cctggggcta ttcaagatgtg tacatgttg aacatcaaga cgggtggtt 360  
 ctcgaggaga ttgttcttac tggccccaa tcatccccgtt accaaaacccc ttctcaaagcc 420  
 ctccaaaaat ggtctccgtt cgaatctgtc ctcgcaccc gccccgcattt gccaaaaga 479

<210> 14  
 <211> 52  
 <212> PRT  
 <213> Glycine max

<400> 14  
 Arg Ser Asn Trp Thr Arg Glu Glu Ile Lys Ala Ile Tyr Asp Lys Pro  
 1 5 10 15  
 Leu Met Glu Leu Cys Trp Gly Ala Gly Ser Leu His Arg Lys Phe His  
 20 25 30

Ile Pro Gly Ala Ile Gln Met Cys Thr Leu Leu Asn Ile Lys Thr Gly  
35 40 45  
Gly Cys Ser Glu  
50

<210> 15  
<211> 589  
<212> DNA  
<213> Triticum aestivum

<220>  
<221> Unsure  
<222> (321)..(321)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (332)..(332)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (335)..(336)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (403)..(403)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (407)..(407)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (516)..(516)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (539)..(539)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (547)..(547)

卷之五

<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (550)..(550)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (555)..(555)  
<223> n = A, C, G, or T

<220>  
<221> Unsure  
<222> (577)..(578)  
<223> n = A, C, G, or T

60  
120  
180  
240  
300  
360  
420  
480  
540  
589

<210> 16  
<211> 78  
<212> PRT  
<213> *Triticum aestivum*

<220>  
<221> UNSURE  
<222> (69)..(69)  
<223> Xaa = any amino acid

```

<400> 16
Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr
1 5 10 15
Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
20 25 30
Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
35 40 45
Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
50 55 60
Glu Leu Gln Glu Xaa Asp Phe Thr Ala Tyr Asn His Asn Leu
65 70 75

```

<210> 17  
 <211> 1396  
 <212> DNA  
 <213> Hordeum vulgare

<400> 17  
 gcaccacaatccctcgcca gtatcgccata gtgcagcagc ggctccgttc cggccagg 60  
 tgctcgccga gcccggccatg atgctgtgtc tcgcgcgcag ctttcgttcc cgcgtccgg 120  
 ccccttcgc ctccggccgtt agcggccgcgc ctttctcata ggtatcgccg ggcgcgggg 180  
 aggccggacgc ggcgggtcgcc gacgggcca ggaacgactg gacccggccc gagatccagg 240  
 ccatacttca gtcggccgtt ctcgacccttt tcttccacgg ggctcaagtc cataggaatg 300  
 tccataataat tagagaatgtt caacaatgtca cactttttt aataaaagact gttgggtgca 360  
 gcgaaagggtt ttcatatgtc ccacagtcc caagatacag taccggattt aaggctgaaa 420  
 aataatgaa gaaagatgtcc gtcctagaag cagctaaaaaa ggcggaaaggag gtcgggagca 480  
 cccgattttt catggggatc gatggggagag agacaattgg cagggaaaca aacttcaacc 540  
 agatcttgcg atatgtcaag gacataaaggat gtatggggatc ggagggtctgt tgcaaccctgg 600  
 gcatgtcaga gaaacacgaa gctgaaagac tcaagaaggc tgacttaca gtttataatc 660  
 ataacctaga tacatcaaga gaatatttac cgaacatctt tcttacaagaatc tgctatgtatc 720  
 atagatcaaa gactcttcg catgtccgtt aagctggaaat aagctgtctgc tcagggtggaa 780  
 ttatgggtt tggagggccg gaggaaaggcc gttgagggtt gttgatataa ctggccactt 840  
 tgccaaacaca cccagagatgtt ccacatgtca atgcattgtatc tgctgtcaaa ggacacgctc 900  
 ttccaggatc gaagccgttgc gatgtatggg aatgtatccg catgttggc agggctccgg 960  
 ttgtatgtcc aaaggcaatg gtgagactt cggcggggcg agtacgggttc tccatggccag 1020  
 agcaacgtttt ctgtttttt gctggggccca actgcattt cgcgggtgaa aagctcttgc 1080  
 caactgtcaaa caacgacttcc gatggggacc aggcaatgtt caagatctt ggctgttattc 1140  
 ccaaggccacc gaaatttggc gatggggagg ccacatgttcc atcatccacg gagatgtgt 1200  
 agcaacgccc ttccatgttcaaa atgttggta tagatgttcc agacccatc cggtcacaaa 1260  
 ctggcacat tatctccacg tagatgttcc tactgttggg atcatgtatc ttgttactcc 1320  
 ctccgttctt aaataataatgtt ctttaagcg atttcaaaaaaaa aaaaaaaaaaaa 1380  
 aaaaaaaaaaaa aaaaaaaaaaaa 1396

<210> 18  
 <211> 405  
 <212> PRT  
 <213> Hordeum vulgare

<400> 18  
 Thr Thr Thr Pro Ser Ala Val Ser Pro Ser Ala Ala Ala Ala Pro Phe  
 1 5 10 15  
 Arg Pro Ala Leu Leu Ala Glu Pro Ala Met Met Leu Leu Leu Ala Arg  
 20 25 30  
 Ser Leu Arg Ser Arg Val Arg Ser Pro Phe Ala Ser Ala Val Ser Ala  
 35 40 45  
 Ala Pro Phe Ser Ser Val Ser Ala Ala Ala Ala Glu Ala Glu Arg Ala  
 50 55 60  
 Val Arg Asp Gly Pro Arg Asn Asp Trp Thr Arg Pro Glu Ile Gln Ala  
 65 70 75 80  
 Ile Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala Gln Val  
 85 90 95  
 His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr Leu Leu  
 100 105 110  
 Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln  
 115 120 125

100 200 300 400 500

Ser	Ser	Arg	Tyr	Ser	Thr	Gly	Leu	Lys	Ala	Glu	Lys	Leu	Met	Lys	Lys	
130						135					140					
Asp	Ala	Val	Leu	Glu	Ala	Ala	Lys	Lys	Ala	Lys	Glu	Ala	Gly	Ser	Thr	
145						150					155				160	
Arg	Phe	Cys	Met	Gly	Ala	Ala	Trp	Arg	Glu	Thr	Ile	Gly	Arg	Lys	Thr	
						165					170				175	
Asn	Phe	Asn	Gln	Ile	Leu	Glu	Tyr	Val	Lys	Asp	Ile	Arg	Gly	Met	Gly	
						180					185				190	
Met	Glu	Val	Cys	Cys	Thr	Leu	Gly	Met	Leu	Glu	Lys	Gln	Gln	Ala	Glu	
						195					200				205	
Glu	Leu	Lys	Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Leu	Asp	Thr		
						210					215				220	
Ser	Arg	Glu	Tyr	Tyr	Pro	Asn	Ile	Ile	Ser	Thr	Arg	Ser	Tyr	Asp	Asp	
						225					230				240	
Arg	Leu	Gln	Thr	Leu	Gln	His	Val	Arg	Glu	Ala	Gly	Ile	Ser	Val	Cys	
						245					250				255	
Ser	Gly	Gly	Ile	Ile	Gly	Leu	Gly	Glu	Ala	Glu	Glu	Asp	Arg	Val	Gly	
						260					265				270	
Leu	Leu	His	Thr	Leu	Ala	Thr	Leu	Pro	Thr	His	Pro	Glu	Ser	Val	Pro	
						275					280				285	
Ile	Asn	Ala	Leu	Ile	Ala	Val	Lys	Gly	Thr	Pro	Leu	Gln	Asp	Gln	Lys	
						290					295				300	
Pro	Val	Glu	Ile	Trp	Glu	Met	Ile	Arg	Met	Ile	Ala	Ser	Ala	Arg	Ile	
						305					310				320	
Val	Met	Pro	Lys	Ala	Met	Val	Arg	Leu	Ser	Ala	Gly	Arg	Val	Arg	Phe	
						325					330				335	
Ser	Met	Pro	Glu	Gln	Ala	Leu	Cys	Phe	Leu	Ala	Gly	Ala	Asn	Ser	Ile	
						340					345				350	
Phe	Ala	Gly	Glu	Lys	Leu	Leu	Thr	Thr	Ala	Asn	Asn	Asp	Phe	Asp	Ala	
						355					360				365	
Asp	Gln	Ala	Met	Phe	Lys	Ile	Leu	Gly	Leu	Ile	Pro	Lys	Ala	Pro	Asn	
						370					375				380	
Phe	Gly	Asp	Glu	Glu	Ala	Thr	Val	Ala	Ser	Ser	Thr	Glu	Arg	Cys	Glu	
						385					390				395	
Gln	Ala	Ala	Ser	Met												
						405										
<210> 19																
<211> 1467																
<212> DNA																
<213> Zea mays																
<400> 19																
gcacgagatcc	aatcggggttgc	cagtttttaa	ggaaaccagg	gaccgcagca	gcaaggccgc										60	
ccagccgacg	aggcgaggag	cgtcaatttc	cgttagctgc	acgaaatccc	tcgaccgtat										120	
cgcccgctgc	tcctctatcc	cttccctgtgt	gtgtctactgt	ccttaagctca	tcactatcat										180	
ggcccttgatg	ctgtctagggc	gcaacctgcg	ctcccgcttc	cgccccacgc	tcgccccgc										240	
cgccggcgatc	tcgtcgccgg	cgccggaggcg	ggagaggcg	atacggacgc	ggccggcgaa										300	
cgactggagc	cggcccccggaa	tccaggccgt	ctacgactca	ccggcttcctcg	accttccttc										360	
tcacgggggct	cgtctatcaa	gatacaacac	tggatggaa	gccccaaaat	tgatgaaacaa										420	
atatgcgttc	tttggaaacgg	caaaaaaggcc	aaaagatgtt	ggggacaccc	gtttttgcatt										480	
ggggatgtca	tggggggaaa	ccatggcgac	aaatccaaac	ttcaaccagg	ttcttgatata										540	
tgtcaaggaa	ataaaggggta	tggcgatgg	ggctctgttc	acactagggca	tgtatagagaa										600	
acacaagaatgt	gaagaactca	agaaggctgg	acttacagca	tataatcata	accttagatca										660	
atcaagagag	tattatccca	acattattac	cacaagatca	tatgtatgtca	gactgcagac										720	

tcttgagcat	gtccgtgaag	ctggaataaag	catctgctca	ggtggaaatca	ttggtcttgg	780
tgaagcagag	gaggacccgg	tagggttgc	geatacccta	gctacccctgc	ctacacaccc	840
agagagcgtt	cctattaatg	cattggttgc	tgtaaaaggc	acaccccttcg	aggaccaga	900
gcctgttagag	atctggaaaa	tgatcccgat	gatccggacta	gctcgatca	cgatgccaa	960
ggcaatggtg	aggcttccag	caggccgagt	acggttctcg	atggcagaa	aaggcgtgb	1020
cttcctcgct	ggggccaaact	ccatcttgc	cgccgagaaa	cttctcacaa	ccgcaaaaca	1080
cgacttgcgt	gcccggccagg	cgatgttca	gatcccttgc	ctgatccca	aggctccaa	1140
ctttggcgat	gaagaggcgt	ctggccgcgc	tcccacagaa	tccgagagg	ctgagcaagc	1200
tgcttcgtat	tagaaatata	acatattatc	accgattata	cgtatcacgg	ttggggcga	1260
actagaatcc	ccgttgtage	tagagcatgt	gatggtagaa	accacaacat	ttcattttat	1320
tgtaaatgt	tgagactgaa	ttggggatac	ccatgtcggg	ctagatcaat	ggacaacttc	1380
cacacaacca	aatccaaaca	ttgaaactca	ttttcatca	cagtttaat	aaacttctcc	1440
cacttatctt	aaaaaaaaaa	aaaaaaaaaa				1467

<210> 20  
<211> 344  
<212> PRT  
<213> Zea mays

<400> 20						
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro						
1 5 10 15						
Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu						
20 25 30						
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile						
35 40 45						
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala						
50 55 60						
Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met Asn						
65 70 75 80						
Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly Ser						
85 90 95						
Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys						
100 105 110						
Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly Met						
115 120 125						
Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln Ala						
130 135 140						
Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp						
145 150 155 160						
Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr Asp						
165 170 175						
Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser Ile						
180 185 190						
Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val						
195 200 205						
Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val						
210 215 220						
Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln						
225 230 235 240						
Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg						
245 250 255						
Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg						
260 265 270						
Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser						

275	280	285
Ile Phe Ala Gly Glu Lys	Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp	
290	295	300
Ala Asp Gln Ala Met Phe Lys	Ile Leu Gly Leu Ile Pro Lys Ala Pro	
305	310	315
Ser Phe Gly Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser Glu		
	325	330
Arg Ser Glu Gln Ala Ala Ser Met		
	340	

<210> 21  
<211> 1515  
<212> DNA  
<213> Zea mays

<210> 22  
<211> 377  
<212> PRT  
<213> *Zea mays*

```

<400> 22
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
1           5           10          15
Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
20          25          30
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile

```



ggggctcagg	tccacagaaa	tgtccataaa	ttcagagaaag	tgcagaatg	cacactttt	360
tcaatcaaga	ctgtggatgt	cagtgaatg	tgtttctact	gtccctgcgc	atcaagatac	420
aacactggat	tgaaaggccca	aaaaatgtat	aaaaatataat	ctgtcttgg	agcagaaaaa	480
aaggcaaaag	agtctggag	caccgtttt	tgcatgggg	ctgcatggg	agaaaccatt	540
ggcggaaat	caaaatccaa	ccagatcttt	gaataatgtca	agaaataaa	ggttatggc	600
atcgaggatct	gttgcacact	aggatgtata	gagaaacaaac	tgatgttga	actcaagaa	660
gtctggactta	cagoatataaa	tcataactca	gatacatcaa	gagatgttt	tcccaaccat	720
attaccacaa	gatcatgtaa	ttagatgtaa	tgatagactg	tgatgttgc	tgaactgtga	780
ataaagcatct	gttcggatgg	aatcattgtt	cagacttttt	atgttttttt	ccgggttaggg	840
tttgttgcata	ccctgtatct	cttgcgttca	caccggaga	ggttttctat	taatgttgc	900
gttgcgtttaa	aaggccaccc	tttttggagac	caaaaggctg	tgatagatgt	ggaaatgtac	960
ccgtatgtatcg	ccactgtctcg	gatccacatg	ccaaaggccaa	ttgtgtgggt	ttcaaggcgc	1020
cgatgtatcggt	ttctggatcc	agaaaaacgg	ttgtgttcc	ttgtgtggc	caacttttt	1080
ttttccggcc	aaaaatcttc	caaaacccga	ttgtgttcc	ttgtgtggc	caacttttt	1140
ttaaagatcc	ttggctgtat	ccccaaatgt	ttgtgttcc	ttgtgtgg	ccaggccatgt	1200
ggcgctccca	caagatccga	ttatccgtat	ttgtgttcc	ttgtgtgg	ggcgcttcgtc	1260
tcatttccga	ttatccgtat	ccagggtgg	ttgtgttcc	ttgtgtgg	tatatacata	1320
cattggatgtt	tagaaaccac	aaatccat	tttttttttt	ttgtgttgc	ttgtgttgc	1380
datatccatcc	tcgggtatca	ttcaatggaca	tttttttttt	ttgtgttgc	ttgtgttgc	1439

```

<210> 24
<211> 377
<212> PRT
<213> Zea mays

<400> 24
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
1 5 10 15
Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
20 25 30
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
35 40 45
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
50 55 60
Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
65 70 75 80
Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
85 90 95
Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
100 105 110
Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
115 120 125
Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
130 135 140
Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
145 150 155 160
Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
165 170 175
Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
180 185 190
Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
195 200 205
Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
210 215 220
Ile Cys Ser Gly Gly Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg

```

225	230	235	240												
Val	Gly	Leu	Leu	His	Thr	Leu	Ala	Thr	Leu	Pro	Thr	His	Pro	Glu	Ser
245	250	255													
Val	Pro	Ile	Asn	Ala	Leu	Val	Ala	Val	Lys	Gly	Thr	Pro	Leu	Glu	Asp
260	265	270													
Gln	Lys	Pro	Val	Glu	Ile	Trp	Glu	Met	Ile	Arg	Met	Ile	Ala	Thr	Ala
275	280	285													
Arg	Ile	Thr	Met	Pro	Lys	Ala	Met	Val	Arg	Leu	Ser	Ala	Gly	Arg	Val
290	295	300													
Arg	Phe	Ser	Met	Pro	Glu	Gln	Ala	Leu	Cys	Phe	Leu	Ala	Gly	Ala	Asn
305	310	315	320												
Ser	Ile	Phe	Ala	Gly	Glu	Lys	Leu	Leu	Thr	Thr	Ala	Asn	Asn	Asp	Phe
325	330	335													
Asp	Ala	Asp	Gln	Ala	Met	Phe	Lys	Ile	Leu	Gly	Leu	Ile	Pro	Lys	Ala
340	345	350													
Pro	Ser	Phe	Gly	Glu	Glu	Glu	Ala	Ser	Ala	Ala	Ala	Pro	Thr	Glu	Ser
355	360	365													
Glu	Arg	Ser	Glu	Gln	Ala	Ala	Ser	Met							
370	375														

<210> 25  
<211> 1477  
<212> DNA  
<213> Argemone mexicana

<400> 25					
gcacgagcat	tcgagaaaata aagagctgta	aaatttttag	ggtttttctg	cataactcta	60
cactcgaa	ttccatataa	gaaatatcat	aaacagaaga	attcaaaaatg	120
aatctttag	agctcgctt	cgaccttta	ttttcatttc	tatctttct	180
catctttt	ttcttcagot	gtctcgcttc	aacgcagaaa	aacgatttaaa	240
gaaacatgg	gaggcagatg	gaaataaaaat	cggtttatgg	ttctccagg	300
tcttcatgg	agctcaagtc	catagacatg	ctcacaactt	cagggaatgt	360
ctcttcctc	tgttaaaggaa	ggtgggttgc	gtgaagatgg	ttcatatgtt	420
ccaggatata	cactggatgt	aaagccccaa	agctgtatga	ccacaatctt	480
cacggaaaa	ggccaaaggag	ggggtagta	cacggttctc	catgggtgt	540
atacagtgg	caggaaagacc	aacttcaaac	agatctctga	gcatggagag	600
gtatggaa	ggggatgtatc	tgactttag	gtatgtatca	atatgtaaaa	660
tcaagcaggc	tgggctcaca	gttttacaaat	atacttcttc	gaaatcttgggg	720
ctaacatcat	caccacaaaga	tcttcatggat	agegcttgg	ttcgccgg	780
aacggatgt	caatgtctgc	tcaggagaaa	taatagggt	aggagaacga	840
gatgttgtt	tttgcatacata	ctagaacacgt	ttccatccaca	tccagaaaatgt	900
atgcattgt	tgcagtcataa	ggcacaccc	tttgcatacata	tttgcatacata	960
agatgattcg	gtatgtatgt	actgtatggaa	tttgcatacata	gaaatatgg	1020
cacggatgt	tgttgcattt	tttgcatacata	aaatgtatgg	gtcaggatgt	1080
atttcattct	cactgtgtat	aaactatgttgc	aaacttccaa	gttgcatttgc	1140
aaatgtatgt	taaggattttgc	gggtgtatgc	aaaaatgtcc	aaatgtatgt	1200
catctttcga	agccgagaga	tgttgcatacata	aacgtatgt	gttgcatttgc	1260
gagattatata	atttaccaaa	atggaaatata	ttccgttccac	tttgcatacata	1320
acatgaatgt	tctttgtatgc	aattatgtaaa	cttccaaat	aaatgtatgt	1380
ggaatgtact	gtctaaattttgc	caattccatg	ggaaatctat	tttgcatacata	1440
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1477

<210> 26  
<211> 379

<212> PRT

<213> Argemone mexicana

<400> 26

Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe  
1 5 10 15  
Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ala Ala  
20 25 30  
Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp  
35 40 45  
Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu  
50 55 60  
Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu  
65 70 75 80  
Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu  
85 90 95  
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys  
100 105 110  
Ala Gln Lys Leu Met Asn Lys Asp Ala Val Leu Gln Ala Ala Glu Lys  
115 120 125  
Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg  
130 135 140  
Asp Thr Val Gly Arg Lys Thr Asn Phe Lys Gln Ile Leu Glu Tyr Val  
145 150 155 160  
Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met  
165 170 175  
Ile Glu Lys Gln Ala Val Glu Leu Lys Gln Ala Gly Leu Thr Ala  
180 185 190  
Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile  
195 200 205  
Thr Thr Arg Ser Tyr Asp Glu Arg Leu Glu Thr Leu Gln Phe Val Arg  
210 215 220  
Glu Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu  
225 230 235 240  
Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro  
245 250 255  
Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly  
260 265 270  
Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg  
275 280 285  
Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu  
290 295 300  
Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe  
305 310 315 320  
Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr  
325 330 335  
Pro Asn Asn Asp Phe Asp Ala Asp Gln Met Met Phe Lys Ile Leu Gly  
340 345 350  
Leu Thr Pro Lys Ala Pro Asn Phe Asp Gln Thr Ser Thr Ser Phe Glu  
355 360 365  
Ala Glu Arg Cys Glu Gln Glu Ala Thr Ala Ser  
370 375

<210> 27

<211> 1526



<212> DNA  
<213> Glycine max

<400> 27  
 gcaacgagcta gtactgtctcc ctctgcgact tcgtttcgta gagggatttt ggccgc当地  
 taaacatgtt caccataaaac tccaaagttcc caacgc当地aa cgaacccaa ccccaacac  
 aaataccgtt gttgttctttt gtctctgtcg tgcttatattt cgcagatctc tcactcatcc  
 tctgttctttt ctctgc当地aa cttcgaattt gaaagc当地aa acatgtttttt ggc当地gaccc  
 attttccgag caccctccctt ttggcgttgg cactcttctt acgcgttattt ctctgc当地ca  
 gcagctgcaaa ttcaagctgaa gagagccatc aaagaaggac ccagaaacgaa ttggagccgaa  
 gaccaagtc当地aa aatccatctt cgaacttccctt attcgc当地tttcttccaa tggggttccaa  
 gttc当地acagacatc ttcaaggaa gttcagc当地gt gtacttttctt gtctt当地aa  
 acaggagggtt gcaacttccaa ttgttccctt tgctcttcaat cctctt当地aa tgatcaggaa  
 gtcaaaaggcc aacgc当地ttttaat gaaacaaaggaa gctgttctt当地aa aggctgaaaggaa  
 gaggttgggaa gcaacttccaa ttgtt当地gggtt gctgttccaa ttgtt当地gggtt  
 accaacttccaa aggatctt tgaatatgtt aaagacatc当地aa ggc当地atggg aatggagg  
 ttgtt当地gggatc ttggcatgtt ggagaaacgaa caggctgttgg aacttcaagaa ggccagg  
 acgttctt当地aa atcacaatctt tgacacttccaa agggatgtt当地aa atcacaacat  
 aggactttagt atgagctt当地aa tcaaaacccctt gagttt当地tttgc当地ggg  
 ttttctt当地gggat gaaatattttt gttt当地gggat gcaaggaggaa atcactttagt  
 acatcttccaa cacttccaa ccatccaggaa agtgttccctt ttaatgtcact ttttctt当地gg  
 aaggaaaccc ttctt当地gggat tcaaaaggcc ttgtt当地aaat gggagatgtt tccgatgata  
 gcaacttccaa gtatcgtt当地aa gcaaaaggaa atgttctt当地aa ttatcgtt当地gg  
 ttctt当地ccatc ttggaggaa attttctt当地gggat gttt当地gggat ttttctt当地gg  
 gaaaaggctt ttaatctt当地aa tcaaaatgtt ttgtt当地gggat atcaacttcat  
 ttggactt当地ccaaaggaa tccaaactt当地aa tcaaaaggaa aaatctt当地gggat  
 tataaggaaag tcaactt当地ttttagtggat ttgtt当地gggat tcaaaacat  
 cttcaactt当地aa tcaattgtt cattttagtggat tacttcatgtt aggttccattt  
 aatctt当地gggat ttttctt当地gggat aacttccaaactt当地aaat aaatatttggaa  
 ttttctt当地aa aaaa  
 1526

<210> 28  
 <211> 415  
 <212> PRT  
 <213> Glycine max

<400> 28  
 Thr Lys Pro Asn Pro Lys His Lys Tyr Arg Cys Cys Leu Leu Ser Leu  
 1 5 10 15  
 Ser Cys Leu Tyr Ser Gln Ile Ser His Ser Phe Ser Val Val Ser Leu  
 20 25 30  
 Pro Asn Phe Glu Phe Glu Ser Lys Asn Met Phe Leu Ala Arg Pro Ile  
 35 40 45  
 Phe Arg Ala Pro Ser Leu Trp Ala Leu His Ser Ser Tyr Ala Tyr Ser  
 50 55 60  
 Ser Ala Ser Ala Ala Ile Gln Ala Glu Arg Ala Ile Lys Glu Gly  
 65 70 75 80  
 Pro Arg Asn Asp Trp Ser Arg Asp Gln Val Lys Ser Ile Tyr Asp Ser  
 85 90 95  
 Pro Ile Leu Asp Leu Leu Phe His Gly Ala Gln Val His Arg His Ala  
 100 105 110  
 His Asn Phe Arg Glu Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr  
 115 120 125  
 Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln Ser Ser Lys Tyr  
 130 135 140

Asp Thr Gly Val Lys Gly Gln Arg Leu Met Asn Lys Glu Ala Val Leu  
 145 150 155 160  
 Gln Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met  
 165 170 175  
 Gly Ala Ala Trp Arg Asp Thr Leu Gly Arg Lys Thr Asn Phe Asn Gln  
 180 185 190  
 Ile Leu Glu Tyr Val Lys Asp Ile Arg Asp Met Gly Met Glu Val Cys  
 195 200 205  
 Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Val Glu Leu Lys Lys  
 210 215 220  
 Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr  
 225 230 235 240  
 Tyr Pro Asn Ile Ile Thr Thr Arg Thr Tyr Asp Glu Arg Leu Gln Thr  
 245 250 255  
 Leu Glu Phe Val Arg Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile  
 260 265 270  
 Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr  
 275 280 285  
 Leu Ser Thr Leu Pro Thr His Pro Glu Ser Val Pro Ile Asn Ala Leu  
 290 295 300  
 Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile  
 305 310 315 320  
 Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys  
 325 330 335  
 Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe Ser Met Pro Glu  
 340 345 350  
 Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu  
 355 360 365  
 Lys Leu Leu Thr Thr Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met  
 370 375 380  
 Phe Lys Val Leu Gly Leu Leu Pro Lys Ala Pro Ser Leu His Glu Gly  
 385 390 395 400  
 Glu Thr Ser Val Thr Glu Asp Tyr Lys Glu Ala Ala Ser Ser Ser  
 405 410 415

<210> 29  
 <211> 1659  
 <212> DNA  
 <213> Glycine max

<400> 29  
 aaagagtta tacagataga tttccaaact ccactcactc accactatgg cgactctcg  
 aactcccta tcaacgatccc tcatcttctt tcgcgtccaaat accccaaac tcgcacccat  
 ctcttccctt gttcgcttca aagtccaaaat gtcgagaaat tatggtagcc tatcatctgt  
 tcctcttcaaat gtcacgaaat catcaacgac atcactatgtt aaggatgtctt accaaaggc  
 actcaacgca actgaacccc gcaagaaatgg gacaagagaa gaaatcaagg cgatctatga  
 taaggcattt atggatgtt gttgggttgc tgtagttt cacaaggaaat tccatatacc  
 tgggttcatat cagatgtta catgtgtaa catcaacgac ggtgttgc cggaggattt  
 ttcttactgc gcccaatcat cccgttacca aacgggttcc aaagcttccaaatgggttcc  
 ctgcgttcaatctt gtcctcgatc cggcccgat cggccaaagac aacgggttca cactgttcttgc  
 catgggagcc gctgtggcgcc atatggcttgc acggaaaacc aatcttcaaaa atgtccaaac  
 aatggatgttgc gagatgttgc gatgttgc gaaatgttgc gtcacgttgc tgatgttgc  
 tgcagacaaat gtccttgc acggaaatgc cgggttccat cacaaggaaatggatgttgc  
 ttcgttgcggg gtttttcatat ccaacggatc cacaaggac accttatgttgc agatgttgc  
 taccatataatgc aatgttgc gaaatggatgttgc acgggttgc tccctggatt

60  
 120  
 180  
 240  
 300  
 360  
 420  
 480  
 540  
 600  
 660  
 720  
 780  
 840

<210> 30

<211> 417

<212> PRT

<213> Glycine max

<400> 30

Met Ala Thr Leu Arg Thr Ser Leu Ser Arg Ser Leu Ile Leu Leu Arg  
 1 5 10 15  
 Ser Asn Thr Pro Lys Leu Ala Pro Ile Ser Ser Ser Val Arg Leu Gln  
 20 25 30  
 Val Gln Lys Ser Arg Asn Tyr Gly Thr Val Ser Ser Val Pro Pro Gln  
 35 40 45  
 Ala Thr Glu Thr Ser Ser Thr Ser Pro Ser Lys Asp Val Tyr Gln Glu  
 50 55 60  
 Ala Leu Asn Ala Thr Glu Pro Arg Ser Asn Trp Thr Arg Glu Glu Ile  
 65 70 75 80  
 Lys Ala Ile Tyr Asp Lys Pro Leu Met Glu Leu Cys Trp Gly Ala Gly  
 85 90 95  
 Ser Leu His Arg Lys Phe His Ile Pro Gly Ala Ile Gln Met Cys Thr  
 100 105 110  
 Leu Leu Asn Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys  
 115 120 125  
 Ala Gln Ser Ser Arg Tyr Gln Thr Gly Leu Lys Ala Ser Lys Met Val  
 130 135 140  
 Ser Val Glu Ser Val Leu Ala Ala Ala Arg Ile Ala Lys Asp Asn Gly  
 145 150 155 160  
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Met Arg Gly Arg  
 165 170 175  
 Lys Thr Asn Leu Lys Asn Val Lys Thr Met Val Ser Glu Ile Arg Gly  
 180 185 190  
 Met Gly Met Glu Val Cys Val Thr Leu Gly Met Ile Asp Ala Gln  
 195 200 205  
 Ala Gln Glu Leu Lys Glu Ala Gly Leu Thr Ala Tyr Asn His Asn Val  
 210 215 220  
 Asp Thr Ser Arg Asp Phe Tyr Pro Lys Val Ile Thr Thr Arg Thr Tyr  
 225 230 235 240  
 Asp Glu Arg Leu Asp Thr Ile Lys Asn Val Arg Glu Ala Gly Ile Asn  
 245 250 255  
 Val Cys Thr Gly Gly Ile Leu Gly Leu Gly Glu Asn Lys Ser Asp His  
 260 265 270

Ile Gly Leu Leu Glu Thr Val Ala Thr Leu Pro Ser His Pro Glu Ser  
 275 280 285  
 Phe Pro Val Asn Met Leu Val Ala Ile Lys Gly Thr Pro Leu Glu Gly  
 290 295 300  
 Asn Lys Lys Val Glu Phe Glu Asn Met Leu Arg Met Val Ala Thr Ala  
 305 310 315 320  
 Arg Ile Val Met Pro Lys Thr Ile Val Arg Leu Ala Ala Gly Arg Gly  
 325 330 335  
 Glu Leu Ser Glu Glu Gln Gln Val Leu Cys Phe Met Ala Gly Ala Asn  
 340 345 350 355  
 Ala Val Phe Thr Gly Glu Thr Met Leu Thr Thr Pro Ala Val Gly Trp  
 355 360 365  
 Gly Val Asp Ser Val Val Phe Asn Arg Trp Gly Leu Arg Pro Met Glu  
 370 375 380  
 Ser Phe Glu Val Glu Ala Leu Lys Asn Asp Lys Pro Ala Thr Thr Asn  
 385 390 395 400  
 Thr Glu Ile Pro Val Glu Ala Ser Lys Ala Glu Met Pro Gly Thr Val  
 405 410 415  
 Ala

TOUCHID=682014/60

<210> 31  
 <211> 1032  
 <212> DNA  
 <213> Triticum aestivum

<400> 31  
 gcacgagaga tgccgtctta gaagcggaaa aaaaggcaaa ggaggctggg agcacccgat 60  
 ttggcatggg agccgcattgg agagagacaa ttggcaggaa aacaaatttc aaccagattc 120  
 ttgaatatgtt caaggacata agaggatgtt gcatggaggct ctgtgcacc ctggcatgc 180  
 tagagaaatca acaagctgaa gaaatcagaaggcttgcactacatccat aatcataacc 240  
 tagatcacatc aagagaataat taccatccaaat ttatccatc aagatcgtac gatgatagat 300  
 tacagactctt tcgatgttgc ctgtgaatgtt gaaataaggcttgcactatccatc 360  
 gtcttggaga ggcggggaaa gaccgtttagt ggctgttgcactacttgcac 420  
 cacatccatc gacgttccatc atcaatgtat tattttgttgcac 480  
 atcagaaggat ttgttgcatgat tggaaatggat tccgcattgttgcac 540  
 tgcccaaggat aatgttgcatgat ttgttgcatgat tgccatgttgcac 600  
 ctctctgtt ctctctgttgcac 660  
 cgaacaatgtt ctctctgttgcac 720  
 ctccaaatctt ctccaaatcttgcac 780  
 ccgtttgtat gttaaatgttgcac 840  
 attcatcgaa attaaatatgg gggatgttgcac 900  
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 960  
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1020  
 aaaaaaaaaaaaaaaa aa 1032

<210> 32  
 <211> 263  
 <212> PRT  
 <213> Triticum aestivum

<400> 32  
 Thr Arg Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly  
 1 5 10 15

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg  
 20 25 30  
 Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly  
 35 40 45  
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln  
 50 55 60  
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu  
 65 70 75 80  
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr  
 85 90 95  
 Asp Asp Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser  
 100 105 110  
 Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg  
 115 120 125  
 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser  
 130 135 140  
 Val Pro Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp  
 145 150 155 160  
 Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala  
 165 170 175  
 Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val  
 180 185 190  
 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn  
 195 200 205  
 Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe  
 210 215 220  
 Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala  
 225 230 235 240  
 Pro Asn Phe Gly Asp Glu Glu Val Met Val Ala Ala Pro Thr Glu Arg  
 245 250 255  
 Cys Glu Gln Ala Ala Leu Met  
 260

<210> 33  
 <211> 378  
 <212> PRT  
 <213> *Arabidopsis thaliana*

<400> 33  
 Met Met Leu Val Arg Ser Val Phe Arg Ser Gln Leu Arg Pro Ser Val  
 1 5 10 15  
 Ser Gly Gly Leu Gln Ser Ala Ser Cys Tyr Ser Ser Leu Ser Ala Ala  
 20 25 30  
 Ser Ala Glu Ala Glu Arg Thr Ile Arg Glu Gly Pro Arg Asn Asp Trp  
 35 40 45  
 Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Leu Leu Asp Leu  
 50 55 60  
 Leu Phe His Gly Ala Gln Val His Arg His Val His Asn Phe Arg Glu  
 65 70 75 80  
 Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu  
 85 90 95  
 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Val Lys  
 100 105 110  
 Ala Gln Arg Leu Met Ser Lys Asp Ala Val Ile Asp Ala Ala Lys Lys  
 115 120 125

Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg  
 130 135 140  
 Asp Thr Ile Gly Arg Lys Thr Asn Phe Ser Gln Ile Leu Glu Tyr Ile  
 145 150 155 160  
 Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met  
 165 170 175  
 Ile Glu Lys Gln Ala Leu Glu Leu Lys Lys Ala Gly Leu Thr Ala  
 180 185 190  
 Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Val Ile  
 195 200 205  
 Thr Thr Arg Ser Tyr Asp Asp Arg Leu Glu Thr Leu Ser His Val Arg  
 210 215 220  
 Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu  
 225 230 235 240  
 Ala Glu Glu Asp Arg Ile Gly Leu Leu His Thr Leu Ala Thr Leu Pro  
 245 250 255  
 Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly  
 260 265 270  
 Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg  
 275 280 285  
 Met Ile Gly Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu  
 290 295 300  
 Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe  
 305 310 315 320  
 Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr  
 325 330 335  
 Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met Phe Lys Thr Leu Gly  
 340 345 350  
 Leu Ile Pro Lys Pro Pro Ser Phe Ser Glu Asp Asp Ser Glu Ser Glu  
 355 360 365  
 Asn Cys Glu Lys Val Ala Ser Ala Ser His  
 370 375

<210> 34  
 <211> 362  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 34  
 Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Phe Phe Ala Leu  
 1 5 10 15  
 Phe Leu Val Arg Asn Asn Trp Thr Arg Glu Glu Ile Gln Lys Ile Tyr  
 20 25 30  
 Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg  
 35 40 45  
 Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Leu Ser Ile  
 50 55 60  
 Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser  
 65 70 75 80  
 Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu  
 85 90 95  
 Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe  
 100 105 110  
 Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe  
 115 120 125

Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu  
 130 135 140  
 Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu  
 145 150 155 160  
 Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg  
 165 170 175  
 Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu  
 180 185 190  
 Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly  
 195 200 205  
 Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile  
 210 215 220  
 His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn  
 225 230 235 240  
 Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu  
 245 250 255  
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile  
 260 265 270  
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys  
 275 280 285  
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val  
 290 295 300  
 Phe Thr Gly Glu Lys Met Leu Leu Leu Leu Phe Leu Asp Ser Asp  
 305 310 315 320  
 Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe Glu  
 325 330 335  
 Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro Pro  
 340 345 350  
 Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu  
 355 360

<210> 35  
 <211> 363  
 <212> PRT  
 <213> Schizosaccharomyces pombe

<400> 35  
 Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Ser Ser Ala Leu  
 1 5 10 15  
 Ser Leu Val Arg Asn Asn Trp Thr Arg Glu Glu Ile Gln Lys Ile Tyr  
 20 25 30  
 Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg  
 35 40 45  
 Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Ser Ile  
 50 55 60  
 Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser  
 65 70 75 80  
 Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu  
 85 90 95  
 Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe  
 100 105 110  
 Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe  
 115 120 125  
 Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu  
 130 135 140

Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu  
 145 150 155 160  
 Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg  
 165 170 175  
 Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu  
 180 185 190  
 Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly  
 195 200 205  
 Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile  
 210 215 220  
 His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn  
 225 230 235 240  
 Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu  
 245 250 255  
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile  
 260 265 270  
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys  
 275 280 285  
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val  
 290 295 300  
 Phe Thr Gly Glu Lys Met Leu Thr Thr Pro Ala Val Ser Trp Asp Ser  
 305 310 315 320  
 Asp Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe  
 325 330 335  
 Glu Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro  
 340 345 350  
 Pro Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu  
 355 360

<210> 36  
 <211> 12  
 <212> PRT  
 <213> biotin synthase conserved sequence element

<220>  
 <221> UNSURE  
 <222> (2)..(2)  
 <223> Xaa represents any amino acid

<220>  
 <221> UNSURE  
 <222> (4)..(4)  
 <223> Xaa represents any amino acid

<220>  
 <221> UNSURE  
 <222> (8)..(8)  
 <223> Xaa represents any amino acid

<220>  
 <221> UNSURE  
 <222> (11)..(11)



223> Xaa represents any amino acid

<400> 36  
Gly Xaa Cys Xaa Glu Asp Cys Xaa Tyr Cys Xaa Gln  
1 5 10

TOEETH0=3320in/60